

SEQUENCE LISTING

<110> Mahajan, Pramod B.
Shi, Jinrui

<120> A Novel Maize Rad51-Like Gene and Uses
Thereof

<130> 1107

<150> 60/132,582
<151> 1999-05-05

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cctaagcgac agcggcgccgg tcgacgttaag cggctgcgtg gcgccaccga cggaggctac	180
gagcgttgtt gtggaggcagat atgagaggtg gaggtggcta caacgggtcg gcggctgtga	240
gatactgaaa tccgcactgc agttctttc ttcccccaat cagtaccacc tctccaagtg	300
gcaatcacc atg gga gat caa tct ggc tct aga aat gga cca caa cag aag	351
Met Gly Asp Gln Ser Gly Ser Arg Asn Gly Pro Gln Gln Lys	
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Tyr Val Ser Gly Ala Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu	
15 20 25 30	

tca cag aaa cac atc act act ggt tct ggt gac ctc aat gac ata ctt	447
Ser Gln Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu	
35 40 45	

ggt ggc ggg att cac tgc aaa gaa gtt act gag atc ggt ggc gtc cca	495
Gly Gly Ile His Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro	
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ggg gtt ggt aaa act caa ctg ggg att caa cta gca atc aat gta caa	543
Gly Val Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln	
65 70 75	

atc cca gtg gaa tgt ggt ggc ctt ggt ggg aaa gca gtt tat ata gat	591
Ile Pro Val Glu Cys Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Asp	
80 85 90	

aca gag ggc agt ttc atg gtt gaa cgt gtc tac cag att gct gaa ggg	639
Thr Glu Gly Ser Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly	
95 100 105 110	

tgt att agg gac ata ctg gag cac ttt ccg cac agc cat gag aag tcc	687
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Cys Ile Arg Asp Ile Leu Glu His Phe Pro His Ser His Glu Lys Ser			
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Ser Ser Val Gln Lys Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile			
130	135	140	
tat tac ttc cggttata tgc agt tac acc gaa caa att gca gtc ata aac			783
Tyr Tyr Phe Arg Ile Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn			
145	150	155	
tac atg gag aag ttc ctc aga gag cat aaa gat gtg cgt ata gtt att			831
Tyr Met Glu Lys Phe Leu Arg Glu His Lys Asp Val Arg Ile Val Ile			
160	165	170	
att gat agt gtt act ttc cac ttt cga caa gat ttt gaa gat ctg gca			879
Ile Asp Ser Val Thr Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala			
175	180	185	190
ctg agg acc aga gtg cta agt gga tta tca ttg aag tta atg aag att			927
Leu Arg Thr Arg Val Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile			
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Ala Lys Thr Tyr Asn Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr			
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aaa ttt aca gaa ggg tca ttt caa ttg act ctt gct cta ggt gac agc			1023
Lys Phe Thr Glu Gly Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser			
225	230	235	
tgg tcc cac tca tgc acg aac cgg ttg att ctg cac tgg aat ggg aac			1071
Trp Ser His Ser Cys Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn			
240	245	250	
gaa cga tac gca cat ctt gat aag tct cct tca ctt cca gta gcc tca			1119
Glu Arg Tyr Ala His Leu Asp Lys Ser Pro Ser Leu Pro Val Ala Ser			
255	260	265	270
gca ccg tat gca gtg aca ggc aaa ggg att aga gat gct gtg agc tca			1167
Ala Pro Tyr Ala Val Thr Gly Lys Gly Ile Arg Asp Ala Val Ser Ser			
275	280	285	
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Asn His Lys Arg Ala Arg Val Thr			
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tgagactgga gaatagtacc attttgta ttctcagttg ctttgtccg ttggctacca			1332
accaacctta agagagaagt aaataacaaca gaacaggcta atatagtgtt ttgtatctga			1392
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Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly		
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Gly Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro		
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Val Glu Cys Gly Gly Leu Gly Lys Ala Val Tyr Ile Asp Thr Glu		
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Gly Ser Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile		
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Arg Asp Ile Leu Glu His Phe Pro His Ser His Glu Lys Ser Ser Ser		
115	120	125
Val Gln Lys Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr		
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Phe Arg Ile Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met		
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Glu Lys Phe Leu Arg Glu His Lys Asp Val Arg Ile Val Ile Ile Asp		
165	170	175
Ser Val Thr Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg		
180	185	190
Thr Arg Val Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys		
195	200	205
Thr Tyr Asn Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe		
210	215	220
Thr Glu Gly Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser		
225	230	240
His Ser Cys Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg		
245	250	255
Tyr Ala His Leu Asp Lys Ser Pro Ser Leu Pro Val Ala Ser Ala Pro		
260	265	270
Tyr Ala Val Thr Gly Lys Gly Ile Arg Asp Ala Val Ser Ser Asn His		
275	280	285
Lys Arg Ala Arg Val Thr		
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gttctttct tcccccaatc agtaccacct ctccaagtgg caatcacc atg gga gat	177
Met Gly Asp	
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caa tct ggc tct aga aat gga cca caa cag aag tac gtt tca gga gcc	225
Gln Ser Gly Ser Arg Asn Gly Pro Gln Gln Lys Tyr Val Ser Gly Ala	
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15	

cag aat gcc tgg gat atg ttc tct gat gag ctg tca cag aaa cac atc	273
Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu Ser Gln Lys His Ile	
20	25
30	35

act act ggt tct ggt gac ctc aat gac ata ctt ggt ggc ggg att cac	321
Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly Ile His	

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tgc aaa gaa gtt act gag atc ggt ggc gtc cca ggg gtt ggt aaa act Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro Gly Val Gly Lys Thr 55	60	65	369
caa ctg ggg att caa cta gca atc aat gta caa atc cca gtg gaa tgt Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro Val Glu Cys 70	75	80	417
ggt ggc ctt ggt ggg aaa gca gtt tat ata gag ggc agt ttc atg gtt Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Glu Gly Ser Phe Met Val 85	90	95	465
gaa cgt gtc tac cag att gct gaa ggg tgt att agg gac ata ctg gag Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile Arg Asp Ile Leu Glu 100	105	110	513
cac ttt ccg cac agc cat gag aag tcc tct tct gtc caa aaa caa tta His Phe Pro His Ser His Glu Lys Ser Ser Val Gln Lys Gln Leu 120	125	130	561
cag cct gag cgt ttc ctg gcg gat atc tat tac ttc cgg ata tgc agt Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr Phe Arg Ile Cys Ser 135	140	145	609
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gag cat aaa gat gtg cgt ata gtt att att gat agt gtt act ttc cac Glu His Lys Asp Val Arg Ile Val Ile Ile Asp Ser Val Thr Phe His 165	170	175	705
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gga tta tca ttg aag tta atg aag att gca aag aca tat aac ttg gca Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys Thr Tyr Asn Leu Ala 200	205	210	801
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caa ttg act ctt gct cta ggt gac agc tgg tcc cac tca tgc acg aac Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser His Ser Cys Thr Asn 230	235	240	897
cgg ttg att ctg cac tgg aat ggg aac gaa cga tac gca cat ctt gat Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg Tyr Ala His Leu Asp 245	250	255	945
aag tct cct tca ctt cca gta gcc tca gcc ccg tat gca gtg aca ggc Lys Ser Pro Ser Leu Pro Val Ala Ser Ala Pro Tyr Ala Val Thr Gly 260	265	270	993
aaa ggg att aga gat gtg tgagctaaaa ccacaagcga gccccgagtaa Lys Gly Ile Arg Asp Val 280			1041

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tttgtgccgt tggctaccaa ccaaccttaa gagagaagta aataacaacag aacaggctaa	1221
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ggcatatatg tgcttctctg atcaccgatc agcaaaaaaaaaaaaaaaa aaaaaaaaaaaa	1341
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Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly	
35 40 45	
Gly Ile His Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro Gly Val	
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Gly Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro	
65 70 75 80	
Val Glu Cys Gly Leu Gly Gly Lys Ala Val Tyr Ile Glu Gly Ser	
85 90 95	
Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile Arg Asp	
100 105 110	
Ile Leu Glu His Phe Pro His Ser His Glu Lys Ser Ser Val Gln	
115 120 125	
Lys Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr Phe Arg	
130 135 140	
Ile Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met Glu Lys	
145 150 155 160	
Phe Leu Arg Glu His Lys Asp Val Arg Ile Val Ile Ile Asp Ser Val	
165 170 175	
Thr Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg Thr Arg	
180 185 190	
Val Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys Thr Tyr	
195 200 205	
Asn Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe Thr Glu	
210 215 220	
Gly Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser His Ser	
225 230 235 240	
Cys Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg Tyr Ala	
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	Met Gly Asp	
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caa tct ggc tct aga aat gga cca caa cag aag tac gtt tca gga gcc		225
Gln Ser Gly Ser Arg Asn Gly Pro Gln Gln Lys Tyr Val Ser Gly Ala		
5 10 15		
cag aat gcc tgg gat atg ttc tct gat gag ctg tca cag aaa cac atc		273
Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu Ser Gln Lys His Ile		
20 25 30 35		
act act ggt tct ggt gac ctc aat gac ata ctt ggt ggc ggg att cac		321
Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly Ile His		
40 45 50		
tgc aaa gaa gtt act gag atc ggt ggc gtc cca ggg gtt ggt aaa act		369
Cys Lys Glu Val Thr Glu Ile Gly Val Pro Gly Val Gly Lys Thr		
55 60 65		
caa ctg ggg att caa cta gca atc aat gta caa atc cca gtg gaa tgt		417
Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro Val Glu Cys		
70 75 80		
ggg ggc ctt ggt ggg aaa gca gtt tat ata gat aca gag ggc agt ttc		465
Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Asp Thr Glu Gly Ser Phe		
85 90 95		
atg gtt gaa cgt gtc tac cag att gct gaa ggg tgt att agg gac ata		513
Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile Arg Asp Ile		
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ctg gag cac ttt ccg cac agc cat gag aag tcc tct tct gtc caa aaa		561
Leu Glu His Phe Pro His Ser His Glu Lys Ser Ser Ser Val Gln Lys		
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caa tta cag cct gag cgt ttc ctg gcg gat atc tat tac ttc cgg ata		609
Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr Phe Arg Ile		
135 140 145		
tgc agt tac acc gaa caa att gca gtc ata aac tac atg gag aag ttc		657
Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met Glu Lys Phe		
150 155 160		
ctc aga gag cat aaa gat gtg cgt ata gtt att att gat agt gtt act		705
Leu Arg Glu His Lys Asp Val Arg Ile Val Ile Ile Asp Ser Val Thr		
165 170 175		
ttc cac ttt cga caa gat ttt gaa gat ctg gca ctg agg acc aga gtg		753
Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg Thr Arg Val		
180 185 190 195		
cta agt gga tta tca ttg aag tta atg aag att gca aag aca tat aac		801
Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys Thr Tyr Asn		
200 205 210		
ttg gca gtt gtc ttg ttg aac caa gtc act act aaa ttt aca gaa ggg		849
Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe Thr Glu Gly		
215 220 225		
tca ttt caa ttg act ctt gct cta ggt gac agc tgg tcc cac tca tgc		897

Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser His Ser Cys			
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acg aac cgg ttg att ctg cac tgg aat ggg aac gaa cga tac gca cat			945
Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg Tyr Ala His			
245	250	255	
ctt gat aag tct cct tca ctt cca gta gcc tca gca ccg tat gca gtg			993
Leu Asp Lys Ser Pro Ser Leu Pro Val Ala Ser Ala Pro Tyr Ala Val			
260	265	270	275
aca ggc aaa ggg att aga gat gct gtg agc tca aac cac aag cga gcc			1041
Thr Gly Lys Gly Ile Arg Asp Ala Val Ser Ser Asn His Lys Arg Ala			
280	285	290	
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Arg Val Thr			
 cctgctgctt tcttcgccat ggatcttttg gactagttagtgg gtgagactgg agaatagtagac			1150
cattttgttg attctcaggtt gctttgtgcc gttggctacc aacccaacctt aagagagaag			1210
taaataacaac agaacaggct aatatagtgt tttgtatctg aacatctggs ccatcgtaaaaaaaaaaaaaaaa			1270
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Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly			
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Gly Ile His Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro Gly Val			
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Gly Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro			
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Val Glu Cys Gly Leu Gly Gly Lys Ala Val Tyr Ile Asp Thr Glu			
85 90 95			
Gly Ser Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile			
100 105 110			
Arg Asp Ile Leu Glu His Phe Pro His Ser His Glu Lys Ser Ser Ser			
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Phe Arg Ile Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met			
145 150 155 160			
Glu Lys Phe Leu Arg Glu His Lys Asp Val Arg Ile Val Ile Ile Asp			
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Ser Val Thr Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg			
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Thr Arg Val Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys			
195 200 205			
Thr Tyr Asn Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe			
210 215 220			
Thr Glu Gly Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser			
225 230 235 240			
His Ser Cys Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg			

245	250	255
Tyr Ala His Leu Asp Lys Ser Pro Ser	Leu Pro Val Ala Ser Ala Pro	
260	265	270
Tyr Ala Val Thr Gly Lys Gly Ile Arg Asp Ala Val Ser Ser Asn His		
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Lys Arg Ala Arg Val Thr		
290		

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<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide based upon an adaptor used for cDNA library construction and poly(dT) to remove clones which have a poly(A) tail but no cDNA insert.

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36

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<212> PRT

<213> Arabidopsis thaliana

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Ile Arg Gly Lys Leu Ile Ser Ala Gly Tyr Thr Cys Leu Ser Ser Ile			
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Ala Ser Val Ser Ser Ser Asp Leu Ala Arg Ala Lys Asn Ala Trp Asp			
50	55	60	
Met Leu His Glu Glu Glu Ser Leu Pro Arg Ile Thr Thr Ser Cys Ser			
65	70	75	80
Asp Leu Asp Asn Ile Leu Gly Gly Ile Ser Cys Arg Asp Val Thr			
85	90	95	
Glu Ile Gly Gly Val Pro Gly Ile Gly Lys Thr Gln Ile Gly Ile Gln			
100	105	110	
Leu Ser Val Asn Val Gln Ile Pro Arg Glu Cys Gly Leu Gly Gly			
115	120	125	
Lys Ala Ile Tyr Ile Asp Thr Glu Gly Ser Phe Met Val Glu Arg Ala			
130	135	140	
Leu Gln Ile Ala Glu Ala Cys Val Glu Asp Met Glu Glu Tyr Thr Gly			
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Tyr Met His His Phe Gln Ala Asn Gln Val Gln Met Lys Pro Glu			
165	170	175	
Asp Ile Leu Glu Asn Ile Phe Tyr Phe Arg Val Cys Ser Tyr Thr Glu			
180	185	190	
Gln Ile Ala Leu Val Asn His Leu Glu Lys Phe Ile Ser Glu Asn Lys			
195	200	205	
Asp Val Val Val Ile Val Asp Ser Ile Thr Phe His Phe Arg Gln Asp			
210	215	220	
Tyr Asp Asp Leu Ala Gln Arg Thr Arg Val Leu Ser Glu Met Ala Leu			
225	230	235	240
Lys Phe Met Lys Leu Ala Lys Lys Phe Ser Leu Ala Val Val Leu Leu			
245	250	255	
Asn Gln Val Thr Thr Lys Phe Ser Glu Gly Ser Phe Gln Leu Ala Leu			
260	265	270	

Ala Leu Gly Asp Ser Trp Ser His Ser Cys Thr Asn Arg Val Ile Leu
275 280 285
Tyr Trp Asn Gly Asp Glu Arg Tyr Ala Tyr Ile Asp Lys Ser Pro Ser
290 295 300
Leu Pro Ser Ala Ser Ala Ser Tyr Thr Val Thr Ser Arg Gly Leu Arg
305 310 315 320
Asn Ser Ser Ser Ser Lys Arg Val Lys Met Met
325 330